

<110> SunGene GmbH & Co.KGaA

<120> DNA-Sequenz kodierend fuer eine
1-Deoxy-D-xylulose-5-phosphat Synthase

<130> 0050/49249

<140> 0817 - 00006

<141> 1999-08-04

<160> 8

<170> PatentIn Vers. 2.0

<210> 1

<211> 2458

<212> DNA

<213> Arabidopsis thaliana

<220>

<221> CDS

<222> (1)..(2154)

<400> 1

atg gct tct tct gca ttt gct ttt cct tct tac ata ata acc aaa gga 48
Met Ala Ser Ser Ala Phe Ala Phe Pro Ser Tyr Ile Ile Thr Lys Gly
1 5 10 15

gga ctt tca act gat tct tgt aaa tca act tct ttg tct tct tct aga 96
Gly Leu Ser Thr Asp Ser Cys Lys Ser Thr Ser Leu Ser Ser Ser Arg
20 25 30

tct ttg gtt aca gat ctt cca tca cca tgt ctg aaa ccc aac aac aat 144
Ser Leu Val Thr Asp Leu Pro Ser Pro Cys Leu Lys Pro Asn Asn Asn
35 40 45

tcc cat tca aac aga aga gca aaa gtg tgt gct tca ctt gca gag aag 192
Ser His Ser Asn Arg Arg Ala Lys Val Cys Ala Ser Leu Ala Glu Lys
50 55 60

ggc gaa tat tat tca aac aga cca cca act cca tta ctt gac act att 240
Gly Glu Tyr Tyr Ser Asn Arg Pro Pro Thr Pro Leu Leu Asp Thr Ile
65 70 75 80

aac tac cca atc cac atg aaa aat ctt tct gtc aag gaa ctg aaa caa 288
Asn Tyr Pro Ile His Met Lys Asn Leu Ser Val Lys Glu Leu Lys Gln

85

90

95

ctt tct gat gag ctg aga tca gac gtg atc ttt aat gtg tcg aaa acc 336
 Leu Ser Asp Glu Leu Arg Ser Asp Val Ile Phe Asn Val Ser Lys Thr
 100 105 110

ggg gga cat ttg ggg tca agt ctt ggt gtt gtg gag ctt act gtg gct 384
 Gly Gly His Leu Gly Ser Ser Leu Gly Val Val Glu Leu Thr Val Ala
 115 120 125

ctt cat tac att ttc aat act cca caa gac aag att ctt tgg gat gtt 432
 Leu His Tyr Ile Phe Asn Thr Pro Gln Asp Lys Ile Leu Trp Asp Val
 130 135 140

ggg cat cag tct tat cct cat aag att ctt act ggg aga aga gga aag 480
 Gly His Gln Ser Tyr Pro His Lys Ile Leu Thr Gly Arg Arg Gly Lys
 145 150 155 160

atg cct aca atg agg caa acc aat ggt ctc tct ggt ttc acc aaa cga 528
 Met Pro Thr Met Arg Gln Thr Asn Gly Leu Ser Gly Phe Thr Lys Arg
 165 170 175

gga gag agt gaa cat gat tgc ttt ggt act gga cac agc tca acc aca 576
 Gly Glu Ser Glu His Asp Cys Phe Gly Thr Gly His Ser Ser Thr Thr
 180 185 190

ata tct gct ggt tta gga atg gcg gta gga agg gat ttg aag ggg aag 624
 Ile Ser Ala Gly Leu Gly Met Ala Val Gly Arg Asp Leu Lys Gly Lys
 195 200 205

aac aac aat gtg gtt gct gtg att ggt gat ggt gcg atg acg gca gga 672
 Asn Asn Asn Val Val Ala Val Ile Gly Asp Gly Ala Met Thr Ala Gly
 210 215 220

cag gct tat gaa gcc atg aac aac gcc gga tat cta gac tct gat atg 720
 Gln Ala Tyr Glu Ala Met Asn Asn Ala Gly Tyr Leu Asp Ser Asp Met
 225 230 235 240

att gtg att ctt aat gac aac aag caa gtc tca tta cct aca gct act 768
 Ile Val Ile Leu Asn Asp Asn Lys Gln Val Ser Leu Pro Thr Ala Thr
 245 250 255

ttg gat gga cca agt cca cct gtt ggt gca ttg agc agt gct ctt agt 816
 Leu Asp Gly Pro Ser Pro Pro Val Gly Ala Leu Ser Ser Ala Leu Ser
 260 265 270

cgg tta cag tct aac ccg gct ctc aga gag ttg aga gaa gtc gca aag 864
 Arg Leu Gln Ser Asn Pro Ala Leu Arg Glu Leu Arg Glu Val Ala Lys

275	280	285	
ggt atg aca aag caa ata ggc gga cca atg cat cag ttg gcg gct aag			912
Gly Met Thr Lys Gln Ile Gly Gly Pro Met His Gln Leu Ala Ala Lys			
290	295	300	
gta gat gtg tat gct cga gga atg ata agc ggt act gga tcg tca ctg			960
Val Asp Val Tyr Ala Arg Gly Met Ile Ser Gly Thr Gly Ser Ser Leu			
305	310	315	320
ttt gaa gaa ctc ggt ctt tac tat att ggt cca gtt gat ggg cac aac			1008
Phe Glu Glu Leu Gly Leu Tyr Tyr Ile Gly Pro Val Asp Gly His Asn			
325	330	335	
ata gat gat ttg gta gcc att ctt aaa gaa gtt aag agt acc aga acc			1056
Ile Asp Asp Leu Val Ala Ile Leu Lys Glu Val Lys Ser Thr Arg Thr			
340	345	350	
aca gga cct gta ctt att cat gtg gtg acg gag aaa ggt cgt ggt tat			1104
Thr Gly Pro Val Leu Ile His Val Val Thr Glu Lys Gly Arg Gly Tyr			
355	360	365	
cct tac gcg gag aga gct gat gac aaa tac cat ggt gtt gtg aaa ttt			1152
Pro Tyr Ala Glu Arg Ala Asp Asp Lys Tyr His Gly Val Val Lys Phe			
370	375	380	
gat cca gca acg ggt aga cag ttc aaa act act aat gag act caa tct			1200
Asp Pro Ala Thr Gly Arg Gln Phe Lys Thr Thr Asn Glu Thr Gln Ser			
385	390	395	400
tac aca act tac ttt gcg gag gca tta gtc gca gaa gca gag gta gac			1248
Tyr Thr Thr Tyr Phe Ala Glu Ala Leu Val Ala Glu Ala Glu Val Asp			
405	410	415	
aaa gat gtg gtt gcg att cat gca gcc atg gga ggt gga acc ggg tta			1296
Lys Asp Val Val Ala Ile His Ala Ala Met Gly Gly Gly Thr Gly Leu			
420	425	430	
aat ctc ttt caa cgt cgc ttc cca aca aga tgt ttc gat gta gga ata			1344
Asn Leu Phe Gln Arg Arg Phe Pro Thr Arg Cys Phe Asp Val Gly Ile			
435	440	445	
gcg gaa caa cac gca gtt act ttt gct gcg ggt tta gcc tgt gaa ggc			1392
Ala Glu Gln His Ala Val Thr Phe Ala Ala Gly Leu Ala Cys Glu Gly			
450	455	460	
ctt aaa ccc ttc tgt gca atc tat tcg tct ttc atg cag cgt gct tat			1440
Leu Lys Pro Phe Cys Ala Ile Tyr Ser Ser Phe Met Gln Arg Ala Tyr			

465	470	475	480	
gac cag gtt gtc cat gat gtt gat ttg caa aaa tta ccg gtg aga ttt				1488
Asp Gln Val Val His Asp Val Asp Leu Gln Lys Leu Pro Val Arg Phe				
	485	490	495	
gca atg gat aga gct gga ctc gtt gga gct gat ggt ccg aca cat tgt				1536
Ala Met Asp Arg Ala Gly Leu Val Gly Ala Asp Gly Pro Thr His Cys				
	500	505	510	
gga gct ttc gat gtg aca ttt atg gct tgt ctt cct aac atg ata gtg				1584
Gly Ala Phe Asp Val Thr Phe Met Ala Cys Leu Pro Asn Met Ile Val				
	515	520	525	
atg gct cca tca gat gaa gca gat ctc ttt aac atg gtt gca act gct				1632
Met Ala Pro Ser Asp Glu Ala Asp Leu Phe Asn Met Val Ala Thr Ala				
	530	535	540	
gtt gcg att gat gat cgt cct tct tgt ttc cgt tac cct aga ggt aac				1680
Val Ala Ile Asp Asp Arg Pro Ser Cys Phe Arg Tyr Pro Arg Gly Asn				
	545	550	555	560
ggt att gga gtt gca tta cct ccc gga aac aaa ggt gtt cca att gag				1728
Gly Ile Gly Val Ala Leu Pro Pro Gly Asn Lys Gly Val Pro Ile Glu				
	565	570	575	
att ggg aaa ggt aga att tta aag gaa gga gag aga gtt gcg ttg ttg				1776
Ile Gly Lys Gly Arg Ile Leu Lys Glu Gly Glu Arg Val Ala Leu Leu				
	580	585	590	
ggt tat ggc tca gca gtt cag agc tgt tta gga gcg gct gta atg ctc				1824
Gly Tyr Gly Ser Ala Val Gln Ser Cys Leu Gly Ala Ala Val Met Leu				
	595	600	605	
gaa gaa cgc gga tta aac gta act gta gcg gat gca cgg ttt tgc aag				1872
Glu Glu Arg Gly Leu Asn Val Thr Val Ala Asp Ala Arg Phe Cys Lys				
	610	615	620	
cca ttg gac cgt gct ctc att cgc agc tta gct aag tcg cac gag gtt				1920
Pro Leu Asp Arg Ala Leu Ile Arg Ser Leu Ala Lys Ser His Glu Val				
	625	630	635	640
ctg atc acg gtt gaa gaa ggt tcc att gga ggt ttt ggc tcg cac gtt				1968
Leu Ile Thr Val Glu Glu Gly Ser Ile Gly Gly Phe Gly Ser His Val				
	645	650	655	
gtt cag ttt ctt gct ctc gat ggt ctt ctt gat ggc aaa ctc aag tgg				2016
Val Gln Phe Leu Ala Leu Asp Gly Leu Leu Asp Gly Lys Leu Lys Trp				

660

665

670

aga cca atg gta ctg cct gat cga tac att gat cac ggt gca cca gct 2064
 Arg Pro Met Val Leu Pro Asp Arg Tyr Ile Asp His Gly Ala Pro Ala
 675 680 685

gat caa cta gct gaa gct gga ctc atg cca tct cac atc gca gca acc 2112
 Asp Gln Leu Ala Glu Ala Gly Leu Met Pro Ser His Ile Ala Ala Thr
 690 695 700

gca ctt aac tta atc ggt gca cca agg gaa gct ctg ttt tga 2154
 Ala Leu Asn Leu Ile Gly Ala Pro Arg Glu Ala Leu Phe
 705 710 715

gagtaagaat ctgttggtta aaacatatgt atacaaacac tctaaatgca acccaagggtt 2214

tcttctaagt actgatcaga attcccgccc gagaagtcct ttggcaacag ctatatatat 2274

ttactaagat tgtgaagaga aaggcaaagg caaagggttg gcaaagatta gtattataga 2334

taaaactggt atttggtttg taattttagg attgtgatga gatcgtgttg taccaataac 2394

taacatcttg taaaatcaat tactctcttg tgatcttcaa taagcttgag tgacaaaaaa 2454

aaaa 2458

<210> 2

<211> 717

<212> PRT

<213> Arabidopsis thaliana

<400> 2

Met Ala Ser Ser Ala Phe Ala Phe Pro Ser Tyr Ile Ile Thr Lys Gly
 1 5 10 15

Gly Leu Ser Thr Asp Ser Cys Lys Ser Thr Ser Leu Ser Ser Ser Arg
 20 25 30

Ser Leu Val Thr Asp Leu Pro Ser Pro Cys Leu Lys Pro Asn Asn Asn
 35 40 45

Ser His Ser Asn Arg Arg Ala Lys Val Cys Ala Ser Leu Ala Glu Lys
 50 55 60

Gly Glu Tyr Tyr Ser Asn Arg Pro Pro Thr Pro Leu Leu Asp Thr Ile
 65 70 75 80

Asn Tyr Pro Ile His Met Lys Asn Leu Ser Val Lys Glu Leu Lys Gln
85 90 95

Leu Ser Asp Glu Leu Arg Ser Asp Val Ile Phe Asn Val Ser Lys Thr
100 105 110

Gly Gly His Leu Gly Ser Ser Leu Gly Val Val Glu Leu Thr Val Ala
115 120 125

Leu His Tyr Ile Phe Asn Thr Pro Gln Asp Lys Ile Leu Trp Asp Val
130 135 140

Gly His Gln Ser Tyr Pro His Lys Ile Leu Thr Gly Arg Arg Gly Lys
145 150 155 160

Met Pro Thr Met Arg Gln Thr Asn Gly Leu Ser Gly Phe Thr Lys Arg
165 170 175

Gly Glu Ser Glu His Asp Cys Phe Gly Thr Gly His Ser Ser Thr Thr
180 185 190

Ile Ser Ala Gly Leu Gly Met Ala Val Gly Arg Asp Leu Lys Gly Lys
195 200 205

Asn Asn Asn Val Val Ala Val Ile Gly Asp Gly Ala Met Thr Ala Gly
210 215 220

Gln Ala Tyr Glu Ala Met Asn Asn Ala Gly Tyr Leu Asp Ser Asp Met
225 230 235 240

Ile Val Ile Leu Asn Asp Asn Lys Gln Val Ser Leu Pro Thr Ala Thr
245 250 255

Leu Asp Gly Pro Ser Pro Pro Val Gly Ala Leu Ser Ser Ala Leu Ser
260 265 270

Arg Leu Gln Ser Asn Pro Ala Leu Arg Glu Leu Arg Glu Val Ala Lys
275 280 285

Gly Met Thr Lys Gln Ile Gly Gly Pro Met His Gln Leu Ala Ala Lys
290 295 300

Val	Asp	Val	Tyr	Ala	Arg	Gly	Met	Ile	Ser	Gly	Thr	Gly	Ser	Ser	Leu
305					310					315					320

Phe Glu Glu Leu Gly Leu Tyr Tyr Ile Gly Pro Val Asp Gly His Asn
325 330 335

Ile Asp Asp	Leu Val Ala	Ile Leu Lys	Glu Val Lys	Ser Thr Arg	Thr
340		345		350	
Thr Gly Pro	Val Leu Ile	His Val Val	Thr Glu Lys	Gly Arg Gly	Tyr
355		360		365	
Pro Tyr Ala	Glu Arg Ala	Asp Asp Lys	Tyr His Gly	Val Val Lys	Phe
370		375		380	
Asp Pro Ala	Thr Gly Arg	Gln Phe Lys	Thr Thr Asn	Glu Thr Gln	Ser
385		390		395	400
Tyr Thr Thr	Tyr Phe Ala	Glu Ala Leu	Val Ala Glu	Ala Glu Val	Asp
	405		410		415
Lys Asp Val	Val Ala Ile	His Ala Ala	Met Gly Gly	Gly Thr Gly	Leu
	420		425		430
Asn Leu Phe	Gln Arg Arg	Phe Pro Thr	Arg Cys Phe	Asp Val Gly	Ile
	435		440		445
Ala Glu Gln	His Ala Val	Thr Phe Ala	Ala Gly Leu	Ala Cys Glu	Gly
	450		455		460
Leu Lys Pro	Phe Cys Ala	Ile Tyr Ser	Ser Phe Met	Gln Arg Ala	Tyr
465		470		475	480
Asp Gln Val	Val His Asp	Val Asp Leu	Gln Lys Leu	Pro Val Arg	Phe
	485		490		495
Ala Met Asp	Arg Ala Gly	Leu Val Gly	Ala Asp Gly	Pro Thr His	Cys
	500		505		510
Gly Ala Phe	Asp Val Thr	Phe Met Ala	Cys Leu Pro	Asn Met Ile	Val
	515		520		525
Met Ala Pro	Ser Asp Glu	Ala Asp Leu	Phe Asn Met	Val Ala Thr	Ala
	530		535		540
Val Ala Ile	Asp Asp Arg	Pro Ser Cys	Phe Arg Tyr	Pro Arg Gly	Asn
545		550		555	560
Gly Ile Gly	Val Ala Leu	Pro Pro Gly	Asn Lys Gly	Val Pro Ile	Glu
	565		570		575
Ile Gly Lys	Gly Arg Ile	Leu Lys Glu	Gly Glu Arg	Val Ala Leu	Leu
	580		585		590

Gly Tyr Gly Ser Ala Val Gln Ser Cys Leu Gly Ala Ala Val Met Leu
 595 600 605

Glu Glu Arg Gly Leu Asn Val Thr Val Ala Asp Ala Arg Phe Cys Lys
 610 615 620

Pro Leu Asp Arg Ala Leu Ile Arg Ser Leu Ala Lys Ser His Glu Val
 625 630 635 640

Leu Ile Thr Val Glu Glu Gly Ser Ile Gly Gly Phe Gly Ser His Val
 645 650 655

Val Gln Phe Leu Ala Leu Asp Gly Leu Leu Asp Gly Lys Leu Lys Trp
 660 665 670

Arg Pro Met Val Leu Pro Asp Arg Tyr Ile Asp His Gly Ala Pro Ala
 675 680 685

Asp Gln Leu Ala Glu Ala Gly Leu Met Pro Ser His Ile Ala Ala Thr
 690 695 700

Ala Leu Asn Leu Ile Gly Ala Pro Arg Glu Ala Leu Phe
 705 710 715

<210> 3

<211> 1863

<212> DNA

<213> Escherichia coli

<220>

<221> CDS

<222> (1)..(1863)

<400> 3

atg agt ttt gat att gcc aaa tac ccg acc ctg gca ctg gtc gac tcc 48
 Met Ser Phe Asp Ile Ala Lys Tyr Pro Thr Leu Ala Leu Val Asp Ser
 1 5 10 15

acc cag gag tta cga ctg ttg ccg aaa gag agt tta ccg aaa ctc tgc 96
 Thr Gln Glu Leu Arg Leu Leu Pro Lys Glu Ser Leu Pro Lys Leu Cys
 20 25 30

gac gaa ctg cgc cgc tat tta ctc gac agc gtg agc cgt tcc agc ggg 144
 Asp Glu Leu Arg Arg Tyr Leu Leu Asp Ser Val Ser Arg Ser Ser Gly
 35 40 45

cac ttc gcc tcc ggg ctg ggc acg gtc gaa ctg acc gtg gcg ctg cac 192

His Phe Ala Ser Gly Leu Gly Thr Val Glu Leu Thr Val Ala Leu His
 50 55 60

tat gtc tac aac acc ccg ttt gac caa ttg att tgg gat gtg ggg cat 240
 Tyr Val Tyr Asn Thr Pro Phe Asp Gln Leu Ile Trp Asp Val Gly His
 65 70 75 80

cag gct tat ccg cat aaa att ttg acc gga cgc cgc gac aaa atc ggc 288
 Gln Ala Tyr Pro His Lys Ile Leu Thr Gly Arg Arg Asp Lys Ile Gly
 85 90 95

acc atc cgt cag aaa ggc ggt ctg cac ccg ttc ccg tgg cgc ggc gaa 336
 Thr Ile Arg Gln Lys Gly Gly Leu His Pro Phe Pro Trp Arg Gly Glu
 100 105 110

agc gaa tat gac gta tta agc gtc ggg cat tca tca acc tcc atc agt 384
 Ser Glu Tyr Asp Val Leu Ser Val Gly His Ser Ser Thr Ser Ile Ser
 115 120 125

gcc gga att ggt att gcg gtt gct gcc gaa aaa gaa ggc aaa aat cgc 432
 Ala Gly Ile Gly Ile Ala Val Ala Ala Glu Lys Glu Gly Lys Asn Arg
 130 135 140

cgc acc gtc tgt gtc att ggc gat ggc gcg att acc gca ggc atg gcg 480
 Arg Thr Val Cys Val Ile Gly Asp Gly Ala Ile Thr Ala Gly Met Ala
 145 150 155 160

ttt gaa gcg atg aat cac gcg ggc gat atc cgt cct gat atg ctg gtg 528
 Phe Glu Ala Met Asn His Ala Gly Asp Ile Arg Pro Asp Met Leu Val
 165 170 175

att ctc aac gac aat gaa atg tcg att tcc gaa aat gtc ggc gcg ctc 576
 Ile Leu Asn Asp Asn Glu Met Ser Ile Ser Glu Asn Val Gly Ala Leu
 180 185 190

aac aac cat ctg gca cag ctg ctt tcc ggt aag ctt tac tct tca ctg 624
 Asn Asn His Leu Ala Gln Leu Leu Ser Gly Lys Leu Tyr Ser Ser Leu
 195 200 205

cgc gaa ggc ggg aaa aaa gtt ttc tct ggc gtg ccg cca att aaa gag 672
 Arg Glu Gly Gly Lys Lys Val Phe Ser Gly Val Pro Pro Ile Lys Glu
 210 215 220

ctg ctc aaa cgc acc gaa gaa cat att aaa ggc atg gta gtg cct ggc 720
 Leu Leu Lys Arg Thr Glu Glu His Ile Lys Gly Met Val Val Pro Gly
 225 230 235 240

acg ttg ttt gaa gag ctg ggc ttt aac tac atc ggc ccg gtg gac ggt 768

Thr	Leu	Phe	Glu	Glu	Leu	Gly	Phe	Asn	Tyr	Ile	Gly	Pro	Val	Asp	Gly	
				245					250					255		
cac	gat	gtg	ctg	ggg	ctt	atc	acc	acg	cta	aag	aac	atg	cgc	gac	ctg	816
His	Asp	Val	Leu	Gly	Leu	Ile	Thr	Thr	Leu	Lys	Asn	Met	Arg	Asp	Leu	
			260					265					270			
aaa	ggc	ccg	cag	ttc	ctg	cat	atc	atg	acc	aaa	aaa	ggt	cgt	ggt	tat	864
Lys	Gly	Pro	Gln	Phe	Leu	His	Ile	Met	Thr	Lys	Lys	Gly	Arg	Gly	Tyr	
		275					280					285				
gaa	ccg	gca	gaa	aaa	gac	ccg	atc	act	ttc	cac	gcc	gtg	cct	aaa	ttt	912
Glu	Pro	Ala	Glu	Lys	Asp	Pro	Ile	Thr	Phe	His	Ala	Val	Pro	Lys	Phe	
	290					295					300					
gat	ccc	tcc	agc	ggt	tgt	ttg	ccg	aaa	agt	agc	ggc	ggt	ttg	ccg	agc	960
Asp	Pro	Ser	Ser	Gly	Cys	Leu	Pro	Lys	Ser	Ser	Gly	Gly	Leu	Pro	Ser	
305				310					315				320			
tat	tca	aaa	atc	ttt	ggc	gac	tgg	ttg	tgc	gaa	acg	gca	gcg	aaa	gac	1008
Tyr	Ser	Lys	Ile	Phe	Gly	Asp	Trp	Leu	Cys	Glu	Thr	Ala	Ala	Lys	Asp	
			325					330					335			
aac	aag	ctg	atg	gcg	att	act	ccg	gcg	atg	cgt	gaa	ggt	tcc	ggc	atg	1056
Asn	Lys	Leu	Met	Ala	Ile	Thr	Pro	Ala	Met	Arg	Glu	Gly	Ser	Gly	Met	
		340					345					350				
gtc	gag	ttt	tca	cgt	aaa	ttc	ccg	gat	cgc	tac	ttc	gac	gtg	gca	att	1104
Val	Glu	Phe	Ser	Arg	Lys	Phe	Pro	Asp	Arg	Tyr	Phe	Asp	Val	Ala	Ile	
		355					360					365				
gcc	gag	caa	cac	gcg	gtg	acc	ttt	gct	gcg	ggt	ctg	gcg	att	ggt	ggg	1152
Ala	Glu	Gln	His	Ala	Val	Thr	Phe	Ala	Ala	Gly	Leu	Ala	Ile	Gly	Gly	
	370					375					380					
tac	aaa	ccc	att	gtc	gcg	att	tac	tcc	act	ttc	ctg	caa	cgc	gcc	tat	1200
Tyr	Lys	Pro	Ile	Val	Ala	Ile	Tyr	Ser	Thr	Phe	Leu	Gln	Arg	Ala	Tyr	
385				390					395					400		
gat	cag	gtg	ctg	cat	gac	gtg	gcg	att	caa	aag	ctt	ccg	gtc	ctg	ttc	1248
Asp	Gln	Val	Leu	His	Asp	Val	Ala	Ile	Gln	Lys	Leu	Pro	Val	Leu	Phe	
			405					410					415			
gcc	atc	gac	cgc	gcg	ggc	att	gtt	ggt	gct	gac	ggt	caa	acc	cat	cag	1296
Ala	Ile	Asp	Arg	Ala	Gly	Ile	Val	Gly	Ala	Asp	Gly	Gln	Thr	His	Gln	
		420					425					430				
ggt	gct	ttt	gat	ctc	tct	tac	ctg	cgc	tgc	ata	ccg	gaa	atg	gtc	att	1344

Gly Ala Phe Asp Leu Ser Tyr Leu Arg Cys Ile Pro Glu Met Val Ile	
435	440 445
atg acc ccg agc gat gaa aac gaa tgt cgc cag atg ctc tat acc ggc	1392
Met Thr Pro Ser Asp Glu Asn Glu Cys Arg Gln Met Leu Tyr Thr Gly	
450	455 460
tat cac tat aac gat ggc ccg tca gcg gtg cgc tac ccg cgt ggc aac	1440
Tyr His Tyr Asn Asp Gly Pro Ser Ala Val Arg Tyr Pro Arg Gly Asn	
465	470 475 480
gcg gtc ggc gtg gaa ctg acg ccg ctg gaa aaa cta cca att ggc aaa	1488
Ala Val Gly Val Glu Leu Thr Pro Leu Glu Lys Leu Pro Ile Gly Lys	
	485 490 495
ggc att gtg aag cgt cgt ggc gag aaa ctg gcg atc ctt aac ttt ggt	1536
Gly Ile Val Lys Arg Arg Gly Glu Lys Leu Ala Ile Leu Asn Phe Gly	
	500 505 510
acg ctg atg cca gaa gcg gcg aaa gtc gcc gaa tcg ctg aac gcc acg	1584
Thr Leu Met Pro Glu Ala Ala Lys Val Ala Glu Ser Leu Asn Ala Thr	
	515 520 525
ctg gtc gat atg cgt ttt gtg aaa ccg ctt gat gaa gcg tta att ctg	1632
Leu Val Asp Met Arg Phe Val Lys Pro Leu Asp Glu Ala Leu Ile Leu	
	530 535 540
gaa atg gcc gcc agc cat gaa gcg ctg gtc acc gta gaa gaa aac gcc	1680
Glu Met Ala Ala Ser His Glu Ala Leu Val Thr Val Glu Glu Asn Ala	
	545 550 555 560
att atg ggc ggc gca ggc agc ggc gtg aac gaa gtg ctg atg gcc cat	1728
Ile Met Gly Gly Ala Gly Ser Gly Val Asn Glu Val Leu Met Ala His	
	565 570 575
cgt aaa cca gta ccc gtg ctg aac att ggc ctg ccg gac ttc ttt att	1776
Arg Lys Pro Val Pro Val Leu Asn Ile Gly Leu Pro Asp Phe Phe Ile	
	580 585 590
ccg caa gga act cag gaa gaa atg cgc gcc gaa ctc ggc ctc gat gcc	1824
Pro Gln Gly Thr Gln Glu Glu Met Arg Ala Glu Leu Gly Leu Asp Ala	
	595 600 605
gct ggt atg gaa gcc aaa atc aag gcc tgg ctg gca taa	1863
Ala Gly Met Glu Ala Lys Ile Lys Ala Trp Leu Ala	
	610 615 620

<210> 4

<211> 620

<212> PRT

<213> Escherichia coli

<400> 4

Met Ser Phe Asp Ile Ala Lys Tyr Pro Thr Leu Ala Leu Val Asp Ser
 1 5 10 15

Thr Gln Glu Leu Arg Leu Leu Pro Lys Glu Ser Leu Pro Lys Leu Cys
 20 25 30

Asp Glu Leu Arg Arg Tyr Leu Leu Asp Ser Val Ser Arg Ser Ser Gly
 35 40 45

His Phe Ala Ser Gly Leu Gly Thr Val Glu Leu Thr Val Ala Leu His
 50 55 60

Tyr Val Tyr Asn Thr Pro Phe Asp Gln Leu Ile Trp Asp Val Gly His
 65 70 75 80

Gln Ala Tyr Pro His Lys Ile Leu Thr Gly Arg Arg Asp Lys Ile Gly
 85 90 95

Thr Ile Arg Gln Lys Gly Gly Leu His Pro Phe Pro Trp Arg Gly Glu
 100 105 110

Ser Glu Tyr Asp Val Leu Ser Val Gly His Ser Ser Thr Ser Ile Ser
 115 120 125

Ala Gly Ile Gly Ile Ala Val Ala Ala Glu Lys Glu Gly Lys Asn Arg
 130 135 140

Arg Thr Val Cys Val Ile Gly Asp Gly Ala Ile Thr Ala Gly Met Ala
 145 150 155 160

Phe Glu Ala Met Asn His Ala Gly Asp Ile Arg Pro Asp Met Leu Val
 165 170 175

Ile Leu Asn Asp Asn Glu Met Ser Ile Ser Glu Asn Val Gly Ala Leu
 180 185 190

Asn Asn His Leu Ala Gln Leu Leu Ser Gly Lys Leu Tyr Ser Ser Leu
 195 200 205

Arg Glu Gly Gly Lys Lys Val Phe Ser Gly Val Pro Pro Ile Lys Glu
 210 215 220

Leu Leu Lys Arg Thr Glu Glu His Ile Lys Gly Met Val Val Pro Gly
 225 230 235 240

Thr Leu Phe Glu Glu Leu Gly Phe Asn Tyr Ile Gly Pro Val Asp Gly
 245 250 255

His Asp Val Leu Gly Leu Ile Thr Thr Leu Lys Asn Met Arg Asp Leu
 260 265 270

Lys Gly Pro Gln Phe Leu His Ile Met Thr Lys Lys Gly Arg Gly Tyr
 275 280 285

Glu Pro Ala Glu Lys Asp Pro Ile Thr Phe His Ala Val Pro Lys Phe
 290 295 300

Asp Pro Ser Ser Gly Cys Leu Pro Lys Ser Ser Gly Gly Leu Pro Ser
 305 310 315 320

Tyr Ser Lys Ile Phe Gly Asp Trp Leu Cys Glu Thr Ala Ala Lys Asp
 325 330 335

Asn Lys Leu Met Ala Ile Thr Pro Ala Met Arg Glu Gly Ser Gly Met
 340 345 350

Val Glu Phe Ser Arg Lys Phe Pro Asp Arg Tyr Phe Asp Val Ala Ile
 355 360 365

Ala Glu Gln His Ala Val Thr Phe Ala Ala Gly Leu Ala Ile Gly Gly
 370 375 380

Tyr Lys Pro Ile Val Ala Ile Tyr Ser Thr Phe Leu Gln Arg Ala Tyr
 385 390 395 400

Asp Gln Val Leu His Asp Val Ala Ile Gln Lys Leu Pro Val Leu Phe
 405 410 415

Ala Ile Asp Arg Ala Gly Ile Val Gly Ala Asp Gly Gln Thr His Gln
 420 425 430

Gly Ala Phe Asp Leu Ser Tyr Leu Arg Cys Ile Pro Glu Met Val Ile
 435 440 445

Met Thr Pro Ser Asp Glu Asn Glu Cys Arg Gln Met Leu Tyr Thr Gly
 450 455 460

Tyr His Tyr Asn Asp Gly Pro Ser Ala Val Arg Tyr Pro Arg Gly Asn
 465 470 475 480

Ala Val Gly Val Glu Leu Thr Pro Leu Glu Lys Leu Pro Ile Gly Lys
 485 490 495

Gly Ile Val Lys Arg Arg Gly Glu Lys Leu Ala Ile Leu Asn Phe Gly
 500 505 510

Thr Leu Met Pro Glu Ala Ala Lys Val Ala Glu Ser Leu Asn Ala Thr
 515 520 525

Leu Val Asp Met Arg Phe Val Lys Pro Leu Asp Glu Ala Leu Ile Leu
 530 535 540

Glu Met Ala Ala Ser His Glu Ala Leu Val Thr Val Glu Glu Asn Ala
 545 550 555 560

Ile Met Gly Gly Ala Gly Ser Gly Val Asn Glu Val Leu Met Ala His
 565 570 575

Arg Lys Pro Val Pro Val Leu Asn Ile Gly Leu Pro Asp Phe Phe Ile
 580 585 590

Pro Gln Gly Thr Gln Glu Glu Met Arg Ala Glu Leu Gly Leu Asp Ala
 595 600 605

Ala Gly Met Glu Ala Lys Ile Lys Ala Trp Leu Ala
 610 615 620

<210> 5

<211> 1469

<212> DNA

<213> Streptomyces avermitilis

<220>

<221> CDS

<222> (218) .. (1138)

<400> 5

gatatccgag cgccgcccggg tccactgcgg tccgaagccg cggatgactc cattcgactg 60

aagccgggtcg agccgcgcct gcacggtgcc gcgcgcgacc ccgagccgcc gggacatctc 120

gagcactccg atgcgcggct cccgcgccag cagcaccagg agccggccgt ccagatgatc 180

gatcgccacg gcagcccctc cagtggatcat cctgtac atg cag ccc cac gcc atg 235

Met Gln Pro His Ala Met

1

5

ggc ggt gca ctg aac aca ttg tcc agc gga caa gcc aac tat tgc gca	283
Gly Gly Ala Leu Asn Thr Leu Ser Ser Gly Gln Ala Asn Tyr Cys Ala	
10 15 20	
cct tgc gga acg gag cga ccc tgc cgc cat gac gca gac cac aca cca	331
Pro Cys Gly Thr Glu Arg Pro Cys Arg His Asp Ala Asp His Thr Pro	
25 30 35	
cac tcc cga cac cgc ccg gca ggc cga ccc ctt ccc ggt gaa ggg aat	379
His Ser Arg His Arg Pro Ala Gly Arg Pro Leu Pro Gly Glu Gly Asn	
40 45 50	
gga cgc ggt cgt ctt cgc cgt agg caa cgc caa gca ggc cgc gca cta	427
Gly Arg Gly Arg Leu Arg Arg Arg Gln Arg Gln Ala Gly Arg Ala Leu	
55 60 65 70	
ctc cac cgc ctt cgg cat gca gct tgt ggc gta ctc cgg acc gga gaa	475
Leu His Arg Leu Arg His Ala Ala Cys Gly Val Leu Arg Thr Gly Glu	
75 80 85	
cgg cag ccg cga gac cgc ttc gta cgt cct cac caa cgg ctc ggc acg	523
Arg Gln Pro Arg Asp Arg Phe Val Arg Pro His Gln Arg Leu Gly Thr	
90 95 100	
ctt cgt cct cac ctc cgt cat caa gcc cgc cac ccc ctg ggg cca ctt	571
Leu Arg Pro His Leu Arg His Gln Ala Arg His Pro Leu Gly Pro Leu	
105 110 115	
cct cgc cga cca tgt ggc cga gca cgg cga cgg cgt cgt cga cct cgc	619
Pro Arg Arg Pro Cys Gly Arg Ala Arg Arg Arg Arg Arg Pro Arg	
120 125 130	
cat cga ggt ccc gga cgc ccg cgc cgc cca cgc gta cgc gat cga gca	667
His Arg Gly Pro Gly Arg Pro Arg Arg Pro Arg Val Arg Asp Arg Ala	
135 140 145 150	
cgg cgc ccg ctc ggt cgc cga gcc gta cga gct gaa gga cga gca cgg	715
Arg Arg Pro Leu Gly Arg Arg Ala Val Arg Ala Glu Gly Arg Ala Arg	
155 160 165	
cac ggt cgt cct cgc cgc gat cgc cac cta cgg caa gac ccg cca cac	763
His Gly Arg Pro Arg Arg Asp Arg His Leu Arg Gln Asp Pro Pro His	
170 175 180	
cct cgt cga ccg gac cgg cta cga cgg ccc cta cct ccc cgg cta cgt	811
Pro Arg Arg Pro Asp Arg Leu Arg Arg Pro Leu Pro Pro Arg Leu Arg	
185 190 195	

ggc cgc cgc ccc gat cgt cga acc gcc cgc cca ccg cac ctt cca ggc 859
 Gly Arg Arg Pro Asp Arg Arg Thr Ala Arg Pro Pro His Leu Pro Gly
 200 205 210

cat cga cca ctg cgt cgg caa cgt cga gct cgg ccg gat gaa cga atg 907
 His Arg Pro Leu Arg Arg Gln Arg Arg Ala Arg Pro Asp Glu Arg Met
 215 220 225 230

ggt cgg ctt cta caa caa ggt cat ggg ctt cac gaa cat gaa gga gtt 955
 Gly Arg Leu Leu Gln Gln Gly His Gly Leu His Glu His Glu Gly Val
 235 240 245

cgt ggg cga cga cat cgc gac cga gta ctc ggc gct gat gtc gaa ggt 1003
 Arg Gly Arg Arg His Arg Asp Arg Val Leu Gly Ala Asp Val Glu Gly
 250 255 260

cgt ggc cga cgg cac gct caa ggt caa gtt ccc gat caa cga gcc cgc 1051
 Arg Gly Arg Arg His Ala Gln Gly Gln Val Pro Asp Gln Arg Ala Arg
 265 270 275

cct cgc caa gaa gaa gtc cca gat cga cga gta cct gga gtt cta cgg 1099
 Pro Arg Gln Glu Glu Val Pro Asp Arg Arg Val Pro Gly Val Leu Arg
 280 285 290

cgg cgc ggg cgt cca gca cat cgc gct gaa cac ggg tga catcgtcgag 1148
 Arg Arg Gly Arg Pro Ala His Arg Ala Glu His Gly
 295 300 305

acggtacgca cgatgcgcgc cgccggcgctc cagttcctgg acacgcccga ctcgtactac 1208

gacaccctcg gggagtgggt gggcgacacc cgcgtccccg tcgacaccct gcgcgagctg 1268

aagatcctcg cggaccgca cgaggacggc tatctgctcc agatcttcac caagccgggtc 1328

caggaccgcc cgacggtctt cttcgagatc atcgaacgcc acggctcgat gggattcggc 1388

aagggcaact tcaaggccct gttcgaggcg atcgagcggg agcaggagaa gcggggcaac 1448

ctgtaggcgg cgcggcccgg g 1469

<210> 6
 <211> 306
 <212> PRT
 <213> Streptomyces avermitilis

<400> 6
 Met Gln Pro His Ala Met Gly Gly Ala Leu Asn Thr Leu Ser Ser Gly

17

260

265

270

Pro Asp Gln Arg Ala Arg Pro Arg Gln Glu Glu Val Pro Asp Arg Arg
 275 280 285

Val Pro Gly Val Leu Arg Arg Arg Gly Arg Pro Ala His Arg Ala Glu
 290 295 300

His Gly
 305

<210> 7

<211> 1479

<212> DNA

<213> Arabidopsis thaliana

<220>

<221> CDS

<222> (1)..(1401)

<400> 7

atg gcg acg acg gtt aca ctc aaa tcc ttc acc gga ctt cgt caa tca 48
 Met Ala Thr Thr Val Thr Leu Lys Ser Phe Thr Gly Leu Arg Gln Ser
 1 5 10 15

tca acg gag caa aca aac ttc gtc tct cat gta ccg tca tca ctt tct 96
 Ser Thr Glu Gln Thr Asn Phe Val Ser His Val Pro Ser Ser Leu Ser
 20 25 30

ctc cct caa cga cgg acc tct ctc cga gta acc gca gcc agg gcc act 144
 Leu Pro Gln Arg Arg Thr Ser Leu Arg Val Thr Ala Ala Arg Ala Thr
 35 40 45

ccc aaa ctc tcc aac cgt aaa ctc cgt gtc gcc gtc atc ggt ggt gga 192
 Pro Lys Leu Ser Asn Arg Lys Leu Arg Val Ala Val Ile Gly Gly Gly
 50 55 60

cca gca ggc ggg gca gct gca gag act cta gca caa gga gga atc gag 240
 Pro Ala Gly Gly Ala Ala Ala Glu Thr Leu Ala Gln Gly Gly Ile Glu
 65 70 75 80

acg att ctc atc gag cgt aag atg gac aat tgc aag cct tgc ggt ggc 288
 Thr Ile Leu Ile Glu Arg Lys Met Asp Asn Cys Lys Pro Cys Gly Gly
 85 90 95

gcg att cct ctc tgt atg gtc gga gaa ttc aac ttg ccg ttg gat att 336
 Ala Ile Pro Leu Cys Met Val Gly Glu Phe Asn Leu Pro Leu Asp Ile

100	105	110	
att gat cgg aga gtg acg aag atg aag atg att tcg ccg tcg aac att			384
Ile Asp Arg Arg Val Thr Lys Met Lys Met Ile Ser Pro Ser Asn Ile			
115	120	125	
gct gtt gat att ggt cgt acg ctt aag gag cat gag tat ata ggt atg			432
Ala Val Asp Ile Gly Arg Thr Leu Lys Glu His Glu Tyr Ile Gly Met			
130	135	140	
gtg aga aga gaa gtt ctt gat gct tat ctg aga gag aga gct gag aag			480
Val Arg Arg Glu Val Leu Asp Ala Tyr Leu Arg Glu Arg Ala Glu Lys			
145	150	155	160
agt gga gcc act gtg att aac ggt ctc ttc ctt aag atg gat cat ccg			528
Ser Gly Ala Thr Val Ile Asn Gly Leu Phe Leu Lys Met Asp His Pro			
	165	170	175
gag aat tgg gac tcg ccg tac act ttg cat tac act gag tac gat ggt			576
Glu Asn Trp Asp Ser Pro Tyr Thr Leu His Tyr Thr Glu Tyr Asp Gly			
	180	185	190
aaa act gga gct aca ggg acg aag aaa aca atg gag gtt gat gct gtc			624
Lys Thr Gly Ala Thr Gly Thr Lys Lys Thr Met Glu Val Asp Ala Val			
195	200	205	
att gga gct gat gga gct aac tct agg gtt gct aaa tct att gat gct			672
Ile Gly Ala Asp Gly Ala Asn Ser Arg Val Ala Lys Ser Ile Asp Ala			
210	215	220	
ggt gat tac gac tac gca att gca ttt cag gag agg att agg att cct			720
Gly Asp Tyr Asp Tyr Ala Ile Ala Phe Gln Glu Arg Ile Arg Ile Pro			
225	230	235	240
gat gag aaa atg act tac tat gag gat tta gct gag atg tat gtt gga			768
Asp Glu Lys Met Thr Tyr Tyr Glu Asp Leu Ala Glu Met Tyr Val Gly			
	245	250	255
gat gat gtg tcg ccg gat ttc tat ggt tgg gtg ttc cct aag tgc gac			816
Asp Asp Val Ser Pro Asp Phe Tyr Gly Trp Val Phe Pro Lys Cys Asp			
260	265	270	
cat gta gct gtt gga aca ggt act gtg act cac aaa ggt gac atc aag			864
His Val Ala Val Gly Thr Gly Thr Val Thr His Lys Gly Asp Ile Lys			
275	280	285	
aag ttc cag ctc gcg acc aga aac aga gct aag gac aag att ctt gga			912
Lys Phe Gln Leu Ala Thr Arg Asn Arg Ala Lys Asp Lys Ile Leu Gly			

290	295	300	
ggg aag atc atc cgt gtg gag gct cat ccg att cct gaa cat ccg aga			960
Gly Lys Ile Ile Arg Val Glu Ala His Pro Ile Pro Glu His Pro Arg			
305	310	315	320
cca cgt agg ctc tcg aaa cgt gtg gct ctt gta ggt gat gct gca ggg			1008
Pro Arg Arg Leu Ser Lys Arg Val Ala Leu Val Gly Asp Ala Ala Gly			
325	330		335
tat gtg act aaa tgc tct ggt gaa ggg atc tac ttt gct gct aag agt			1056
Tyr Val Thr Lys Cys Ser Gly Glu Gly Ile Tyr Phe Ala Ala Lys Ser			
340	345		350
gga aga atg tgt gct gaa gcc att gtc gaa ggt tca cag aat ggt aag			1104
Gly Arg Met Cys Ala Glu Ala Ile Val Glu Gly Ser Gln Asn Gly Lys			
355	360		365
aag atg att gac gaa ggg gac ttg agg aag tac ttg gag aaa tgg gat			1152
Lys Met Ile Asp Glu Gly Asp Leu Arg Lys Tyr Leu Glu Lys Trp Asp			
370	375		380
aag aca tac ttg cct acc tac agg gta ctt gat gtg ttg cag aaa gtg			1200
Lys Thr Tyr Leu Pro Thr Tyr Arg Val Leu Asp Val Leu Gln Lys Val			
385	390	395	400
ttt tac aga tca aat ccg gct aga gaa gcg ttt gtg gag atg tgt aat			1248
Phe Tyr Arg Ser Asn Pro Ala Arg Glu Ala Phe Val Glu Met Cys Asn			
405	410		415
gat gag tat gtt cag aag atg aca ttc gat agc tat ctg tac aag cgg			1296
Asp Glu Tyr Val Gln Lys Met Thr Phe Asp Ser Tyr Leu Tyr Lys Arg			
420	425		430
gtt gcg ccg ggt agt cct ttg gag gat atc aag ttg gct gtg aac acc			1344
Val Ala Pro Gly Ser Pro Leu Glu Asp Ile Lys Leu Ala Val Asn Thr			
435	440		445
att gga agt ttg gtt agg gct aat gct cta agg aga gag att gag aag			1392
Ile Gly Ser Leu Val Arg Ala Asn Ala Leu Arg Arg Glu Ile Glu Lys			
450	455		460
ctt agt gtt taagaaacaa ataatgaggt ctatctcctt tcttcatctc			1441
Leu Ser Val			
465			
tatctctcctt tttttgtctg ttagtaatct atctacac			1479

<210> 8

<211> 467

<212> PRT

<213> Arabidopsis thaliana

<400> 8

Met Ala Thr Thr Val Thr Leu Lys Ser Phe Thr Gly Leu Arg Gln Ser
 1 5 10 15

Ser Thr Glu Gln Thr Asn Phe Val Ser His Val Pro Ser Ser Leu Ser
 20 25 30

Leu Pro Gln Arg Arg Thr Ser Leu Arg Val Thr Ala Ala Arg Ala Thr
 35 40 45

Pro Lys Leu Ser Asn Arg Lys Leu Arg Val Ala Val Ile Gly Gly Gly
 50 55 60

Pro Ala Gly Gly Ala Ala Ala Glu Thr Leu Ala Gln Gly Gly Ile Glu
 65 70 75 80

Thr Ile Leu Ile Glu Arg Lys Met Asp Asn Cys Lys Pro Cys Gly Gly
 85 90 95

Ala Ile Pro Leu Cys Met Val Gly Glu Phe Asn Leu Pro Leu Asp Ile
 100 105 110

Ile Asp Arg Arg Val Thr Lys Met Lys Met Ile Ser Pro Ser Asn Ile
 115 120 125

Ala Val Asp Ile Gly Arg Thr Leu Lys Glu His Glu Tyr Ile Gly Met
 130 135 140

Val Arg Arg Glu Val Leu Asp Ala Tyr Leu Arg Glu Arg Ala Glu Lys
 145 150 155 160

Ser Gly Ala Thr Val Ile Asn Gly Leu Phe Leu Lys Met Asp His Pro
 165 170 175

Glu Asn Trp Asp Ser Pro Tyr Thr Leu His Tyr Thr Glu Tyr Asp Gly
 180 185 190

Lys Thr Gly Ala Thr Gly Thr Lys Lys Thr Met Glu Val Asp Ala Val
 195 200 205

Ile Gly Ala Asp Gly Ala Asn Ser Arg Val Ala Lys Ser Ile Asp Ala
 210 215 220

Gly Asp Tyr Asp Tyr Ala Ile Ala Phe Gln Glu Arg Ile Arg Ile Pro
225 230 235 240

Asp Glu Lys Met Thr Tyr Tyr Glu Asp Leu Ala Glu Met Tyr Val Gly
245 250 255

Asp Asp Val Ser Pro Asp Phe Tyr Gly Trp Val Phe Pro Lys Cys Asp
260 265 270

His Val Ala Val Gly Thr Gly Thr Val Thr His Lys Gly Asp Ile Lys
275 280 285

Lys Phe Gln Leu Ala Thr Arg Asn Arg Ala Lys Asp Lys Ile Leu Gly
290 295 300

Gly Lys Ile Ile Arg Val Glu Ala His Pro Ile Pro Glu His Pro Arg
305 310 315 320

Pro Arg Arg Leu Ser Lys Arg Val Ala Leu Val Gly Asp Ala Ala Gly
325 330 335

Tyr Val Thr Lys Cys Ser Gly Glu Gly Ile Tyr Phe Ala Ala Lys Ser
340 345 350

Gly Arg Met Cys Ala Glu Ala Ile Val Glu Gly Ser Gln Asn Gly Lys
355 360 365

Lys Met Ile Asp Glu Gly Asp Leu Arg Lys Tyr Leu Glu Lys Trp Asp
370 375 380

Lys Thr Tyr Leu Pro Thr Tyr Arg Val Leu Asp Val Leu Gln Lys Val
385 390 395 400

Phe Tyr Arg Ser Asn Pro Ala Arg Glu Ala Phe Val Glu Met Cys Asn
405 410 415

Asp Glu Tyr Val Gln Lys Met Thr Phe Asp Ser Tyr Leu Tyr Lys Arg
420 425 430

Val Ala Pro Gly Ser Pro Leu Glu Asp Ile Lys Leu Ala Val Asn Thr
435 440 445

Ile Gly Ser Leu Val Arg Ala Asn Ala Leu Arg Arg Glu Ile Glu Lys
450 455 460

Leu Ser Val
465